

Serial No.: 10/552,857

Response to Office Action mailed: February 18, 2010

Amendment Dated: August 18, 2010

**Amendments to the specification:**

**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims:**

1-64. (canceled)

65. (currently amended) A nucleic acid construct comprising
- a first nucleic acid portion encoding a chalcone synthase (CHS), or complementary or antisense to a sequence encoding CHS, said first nucleic acid portion comprising a nucleotide sequence selected from the group consisting of
- (a) Sequence ID Nos. 1, 3, 5 and 7,
  - (b) nucleotide sequences encoding Sequence ID Nos. 2, 4, 6 and 8;
  - (c) full-length complements of the sequences recited in (a) and (b);
  - (d) full-length sequences antisense to the sequences recited in (a), and (b) and (c);
  - (e) functionally active fragments of the sequences recited in (a), (b), (c) and (d),
- said functionally active fragments having a size of at least 60 nucleotides;
- (f) functionally active fragments and variants of the sequences recited in (a), (b), (c) and (d), said functionally active variants having at least 90% identity to the relevant part of the sequences~~sequence~~ recited in (a), (b), (c) ~~[[and]]~~or (d), ~~respectively;~~ and
- ~~[[ (f) ]]~~(g) RNA sequences corresponding to the sequences recited in (a), (b), (c), (d), ~~[[and]]~~ (e), and (f); and
- a second nucleic acid portion encoding a dihydroflavonol 4-reductase (BAN), or complementary or antisense to a sequence encoding BAN, said second nucleic acid portion comprising a nucleotide sequence selected from the group consisting of
- (a) Sequence ID No. 9;

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(b) nucleotide sequences encoding Sequence ID No. 10;

(c) full-length complements of the sequences recited in (a) and (b);

(d) full-length sequences antisense to the sequences recited in (a), (b) and (c); and

(e) functionally active fragments of the sequences recited in (a), (b), (c) and (d),

said functionally active fragments having a size of at least 60 nucleotides;

(f) functionally active variants of the sequences recited in (a), (b), (c) and (d), said

functionally active [[and]]variants having at least 90% identity to the relevant part of the  
sequences sequence recited in (a), (b), (c) [[and]] or (d), respectively; and

[[f]](g) RNA sequences corresponding to the sequences recited in (a), (b), (c),

(d), [[and]] (e), and (f); said construct modifying the levels of both the CHS and the BAN when  
the construct is introduced into a plant cell.

66. (currently amended) The nucleic acid construct according to Claim 65, further  
comprising a third nucleic acid portion encoding a leucoanthocyanidine reductase (LAR), or  
complementary or antisense to a sequence encoding LAR, said third nucleic acid portion  
comprising a nucleotide sequence selected from the group consisting of

(a) Sequence ID Nos. 11, 13 and 15;

(b) nucleotide sequences encoding Sequence ID Nos. 12, 14 and 16;

(c) full-length complements of the sequences recited in (a) and (b);

(d) full-length sequences antisense to the sequences recited in (a), (b) and (c);

[[and]]

(e) functionally active fragments of the sequences recited in (a), (b), (c) and (d),

said functionally active fragments having a size of at least 60 nucleotides;

(f) functionally active [[and]]variants of the sequences recited in (a), (b), (c) and

(d), said functionally active variants having at least 90% identity to the sequence recited in (a),  
(b), (c) or (d), respectively; and

[[f]](g) RNA sequences corresponding to the sequences recited in (a), (b), (c),

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(d), ~~[[and]]~~ (e), and (f); said construct modifying the levels of each of the CHS, the BAN and the LAR when the construct is introduced into a plant cell.

67. (currently amended) The nucleic acid construct according to ~~claim~~Claim 65 wherein said functionally active ~~fragments and variants~~ have at least approximately 95% identity to the relevant part of the sequences recited in (a), (b), (c) ~~[[and]]~~or (d), respectively, ~~and have a size of at least 60 nucleotides.~~

68. (currently amended) The nucleic acid construct according to ~~claim~~Claim 65 wherein said first nucleic acid portion comprises a nucleotide sequence selected from the group consisting of

- (a) Sequence ID Nos. 1, 3, 5 and 7;
- (b) nucleotide sequences encoding Sequence ID Nos. 2, 4, 6 and 8;
- (c) full-length complements of the sequences recited in (a) and (b);
- (d) full-length sequences antisense to the sequences recited in (a), (b) and (c); and
- (e) RNA sequences corresponding to the sequences recited in (a), (b), (c), (d) and

(e); and

said second nucleic acid portion comprises a nucleotide sequence selected from the group consisting of

- (a) Sequence ID No. 9;
- (b) nucleotide sequences encoding Sequence ID No. 10;
- (c) full-length complements of the sequences recited in (a) and (b);
- (d) full-length sequences antisense to the sequences recited in (a), ~~(b) and (b) and~~

(c); and

(e) full-length RNA sequences corresponding to the sequences recited in (a), (b), (c) ~~[[,]]~~ and (d) and (e).

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69. (currently amended) A plant cell, plant, plant seed or other plant part, having incorporated therein the nucleic acid ~~[[a ]]~~construct according to ~~Claims 62~~Claim 65.

70. (currently amended) A plant, plant seed or other plant part derived from the plant cell or plant according to Claim 69 and having incorporated therein a nucleic acid construct comprising a first nucleic acid portion encoding a chalcone synthase (CHS), or complementary or antisense to a sequence encoding CHS, said first nucleic acid portion comprising a nucleotide sequence selected from the group consisting of

(a) Sequence ID Nos. 1, 3, 5 and 7;

(b) nucleotide sequences encoding Sequence ID Nos. 2, 4, 6 and 8;

(c) full-length complements of the sequences recited in (a) and (b);

(d) full-length sequences antisense to the sequences recited in (a), (b) and (c);

(e) functionally active fragments of the sequences recited in (a), (b), (c) and (d),

said functionally active fragments having a size of at least 60 nucleotides;

(f) functionally active variants of the sequences recited in (a), (b), (c) and (d), said functionally active variants having at least 90% identity to the sequence recited in (a), (b), (c) or (d), respectively; and

(g) RNA sequences corresponding to the sequences recited in (a), (b), (c), (d), (e) and (f); and

from a *Trifolium* species and a second nucleic acid portion encoding a dihydroflavonol 4-reductase (BAN) from a *Trifolium* species, or complementary or antisense to a sequence encoding BAN, said second nucleic acid portion comprising a nucleotide sequence selected from the group consisting of

(a) Sequence ID No. 9;

(b) nucleotide sequences encoding Sequence ID No. 10;

(c) full-length complements of the sequences recited in (a) and (b);

(d) full-length sequences antisense to the sequences recited in (a), (b) and (c);

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(e) functionally active fragments of the sequences recited in (a), (b), (c) and (d), said functionally active fragments having a size of at least 60 nucleotides;

(f) functionally active variants of the sequences recited in (a), (b), (c) and (d), said functionally active variants having at least 90% identity to the sequence recited in (a), (b), (c) or (d), respectively; and

(g) RNA sequences corresponding to the sequences recited in (a), (b), (c), (d), (e) and (f); said construct ~~expressing~~modifying the levels of both the CHS and the BAN when the construct is introduced into a plant cell.

71. (currently amended) A method of modifying one or more processes selected from the group consisting of condensed tannin biosynthesis; protein binding; metal chelation; anti oxidation; UV-light absorption; and plant defense to a biotic stress in a plant, said method ~~including~~ comprising introducing into said plant an effective amount of ~~[[a ]]~~the nucleic acid construct according to ~~claim 62~~Claim 65.

72. (previously presented) The method according to Claim 71, wherein the method comprises modifying plant defense to biotic stress and the biotic stress is selected from the group consisting of viruses, micro-organisms, insects and fungal pathogens.

73. (currently amended) The method according to claim 71 wherein said nucleic acid construct further comprises a third nucleic acid portion encoding leucoanthocyanidine reductase (LAR), or complementary or antisense to a sequence encoding LAR, said third nucleic acid portion comprising a nucleotide sequence selected from the group consisting of~~from a~~ Trifolium species

(a) Sequence ID Nos. 11, 13 and 15;

(b) nucleotide sequences encoding Sequence ID Nos. 12, 14 and 16;

(c) full-length complements of the sequences recited in (a) and (b);

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(d) full-length sequences antisense to the sequences recited in (a), (b) and (c);

(e) functionally active fragments of the sequences recited in (a), (b), (c) and (d),  
said functionally active fragments having a size of at least 60 nucleotides;

(f) functionally active variants of the sequences recited in (a), (b), (c), and (d), said  
functionally active variants having at least 90% identity to the sequence recited in (a), (b), (c) or  
(d), respectively; and

(g) RNA seqneces corresponding to the sequences recited in (a), (b), (c), (d), (e)  
and (f); said construct modifying the levels of each of the CHS, the BAN and the LAR when the  
construct is introduced into a plant cell.

74. (cancelled)

75. (currently amended) A method of modifying forage quality of a plant by disrupting protein foam and/or conferring protection from rumen pasture bloat, said method **including** comprising introducing into said plant an effective amount of [[a ]]the nucleic acid construct according to Claim [[62]]65.

76. (currently amended) The method according to claim 75 wherein said nucleic acid construct further comprises a third nucleic acid portion encoding leucoanthocyanidine reductase (LAR) from a Trifolium species, or complementary or antisense to a sequence encoding LAR, said third nucleic acid portion comprising a nucleotide sequence selected from the group consisting of

(a) Sequence ID Nos. 11, 13 and 15;

(b) nucleotide sequences encoding Sequence ID Nos. 12, 14 and 16;

(c) full-length complements of the sequences recited in (a) and (b);

(d) full-length sequences antisense to the sequences recited in (a), (b) and (c);

(e) functionally active fragments of the sequences recited in (a), (b), (c) and (d),

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said functionally active fragments having a size of at least 60 nucleotides;

(f) functionally active variants of the sequences recited in (a), (b), (c) and (d), said functionally active variants having at least 90% identity to the sequence recited in (a), (b), (c) or (d), respectively; and

(g) RNA sequences corresponding to the sequences recited in (a), (b), (c), (d), (e) and (f); said construct modifying the levels of each of the CHS, the BAN and the LAR when the construct is introduced into a plant cell.

77. (new) A nucleic acid construct comprising

a first nucleic acid portion encoding a chalcone synthase (CHS), or complementary or antisense to a sequence encoding CHS, said first nucleic acid portion comprising a nucleotide sequence selected from the group consisting of

(a) Sequence ID No. 1;

(b) nucleotide sequences encoding Sequence ID No. 2;

(c) full-length complements of the sequences recited in (a) and (b);

(d) full-length sequences antisense to the sequences recited in (a), (b) and (c);

(e) functionally active fragments of the sequences recited in (a), (b), (c) and (d),

said functionally active fragments having a size of at least 60 nucleotides;

(f) functionally active variants of the sequences recited in (a), (b), (c) and (d), said functionally active variants having at least 90% identity to the sequence recited in (a), (b), (c) or (d), respectively; and

(g) RNA sequences corresponding to the sequences recited in (a), (b), (c), (d), (e) and (f); and

a second nucleic acid portion encoding a dihydroflavanol 4-reductase (BAN), or complementary or antisense to a sequence encoding BAN, said second nucleic acid portion comprising a nucleotide sequence selected from the group consisting of

(a) Sequence ID No. 9;

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(b) nucleotide sequences encoding Sequence ID No. 10;

(c) full-length complements of the sequences recited in (a) and (b);

(d) full-length sequences antisense to the sequences recited in (a), (b) and (c);

(e) functionally active fragments of the sequences recited in (a), (b), (c) and (d),

said functionally active fragments having a size of at least 60 nucleotides;

(f) functionally active variants of the sequences recited in (a), (b), (c) and (d), said

functionally active variants having at least 90% identity to the sequence recited in (a), (b), (c) or (d), respectively; and

(g) RNA sequences corresponding to the sequences recited in (a), (b), (c), (d), (e)

and (f); said construct modifying the levels of both the CHS and the BAN when the construct is introduced into a plant cell.

78. (new) The nucleic acid construct according to Claim 77, further comprising a third nucleic acid portion encoding a leucoanthocyanidine reductase (LAR), or complementary or antisense to a sequence encoding LAR, said third nucleic acid portion comprising a nucleotide sequence selected from the group consisting of

(a) Sequence ID No. 11;

(b) nucleotide sequences encoding Sequence ID No. 12;

(c) full-length complements of the sequences recited in (a) and (b);

(d) full-length sequences antisense to the sequences recited in (a), (b) and (c);

(e) functionally active fragments of the sequences recited in (a), (b), (c) and (d),

said functionally active fragments having a size of at least 60 nucleotides;

(f) functionally active variants of the sequences recited in (a), (b), (c) and (d), said

functionally active variants having at least 90% identity to the sequence recited in (a), (b), (c) or (d), respectively; and

(g) RNA sequences corresponding to the sequences recited in (a), (b), (c), (d), (e)

and (f); said construct modifying the levels of each of the CHS, the BAN and the LAR when the



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construct is introduced into a plant cell.

79. (new) The nucleic acid construct according to Claim 77 wherein said functionally active variants have at least approximately 95% identity to the sequence recited in (a), (b), (c) or (d), respectively.

80. (new) The nucleic acid construct according to Claim 79 wherein said functionally active variants comprise variants of the sequences recited in (a), (b), (c) and (d) with one or more nucleotide changes that result in conservative amino acid substitution.

81. (new) The nucleic acid construct according to claim 77 wherein  
said first nucleic acid portion comprises a nucleotide sequence selected from the group  
consisting of

- (a) Sequence ID No. 1;
- (b) nucleotide sequences encoding Sequence ID No. 2;
- (c) full-length complements of the sequences recited in (a) and (b);
- (d) full-length sequences antisense to the sequences recited in (a), (b) and (c); and
- (e) RNA sequences corresponding to the sequences recited in (a), (b), (c) and

(d); and

said second nucleic acid portion comprises a nucleotide sequence selected from the group  
consisting of

- (a) Sequence ID No. 9;
- (b) nucleotide sequences encoding Sequence ID No. 10;
- (c) full-length complements of the sequences recited in (a) and (b);
- (d) full-length sequences antisense to the sequences recited in (a), (b) and (c); and
- (e) full-length RNA sequences corresponding to the sequences recited in (a), (b),

(c) and (d).

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82. (new) The nucleic acid construct according to Claim 67 wherein said functionally active variants comprise variants of the sequences recited in (a), (b), (c) and (d) with one or more nucleotide changes that result in conservative amino acid substitutions.